

SEQUENCE LISTING

<110> Devgen N.V.

5

Devgen N.V.

10 <120> Kinase sequences useful for developing compounds for the prevention and/or treatment of metabolic diseases and nucleotide sequences encoding such kinase sequences.

<130> P 02-011

15

<160> 13

<170> PatentIn version 3.1

<210> 1

20

<211> 2949

<212> DNA

25

<213> Caenorhabditis elegans

<400> 1

	atggcgctg cegtcttaca aaaacccggt gttatcaagg atccatcgat tgctgcattg	60
30	ttcagtaata aggatccaga gcagagatat caagatttaa gagaaattgg acatggatct	120
	tttggagctg tctattttgc atatgacaaa aaaaatgagc agactgttgc gattaaaaag	180
	atgaatttta gtggaaaaca ggctgtcgaa aatggaatg atattcttaa agaagtgtct	240
35	tttctgaata cagttgttca tccacatatt gtcgactaca aggcttgttt tcttaaggac	300
	actacatgtt ggcttgtgat ggagtactgt attggctctg cagccgatat agtggatgtc	360
40	ttgcgaaaag gaatgcgaga agtcgaaatc gctgcgattt gctctcaaac tttggatgct	420
	cttcgatatc ttcactctct gaagcgaata catcgagata ttaaagctgg aaatattctg	480
	ctatctgata atgctattgt taaactagct gatttcggat ccgcatccct ggtagatccg	540
45	gctcaaactt tcatcggaac gccgtttttc atggccccag aggtaattct ggcaatggat	600
	gagggtcact acacggatcg tgcagatatt tggtcattgg gtatcacgtg tatagagctg	660
50	gccgaacgtc gtccaccatt gttcagtatg aatgcaatgt ctgccctcta ccatattgct	720
	caaaatgata ctccaactct ttctccaatt gacactagcg aacaaccgga atggtcgctg	780
	gaattcgttc aatttataga caaatgtctt cgaaaaccag cagaagagcg aatgtcagct	840
55	gaagaatgct ttcgacatcc attcattcaa cggctctcgcc catcagacac aattcaggaa	900

ctcattcaga gaacgaaaaa tatggtatta gagttggata attttcaata caaaaagatg 960
agaaaactca tgtatttggga tgaaacagaa ggaaaagaag gaagtgaagg aaatggagca 1020
5 tctgatgatt tagattttca tggaaatgaa gctaattcaa ttggaagagc aggagattct 1080
gcgtcatctc gaagtgcttc tcttacttct ttcgatcaa tgcagagtag tggaggagct 1140
ggctcttttag tgtccaccaa tacgacgggt gctatggata atgtgcatgg atcctctgga 1200
10 tacggtaatg gaagtagttc gacgacgagc tccgcacgcc gccgtcctcc aattccttcg 1260
caaatgctct cttctacatc aacgtctggg gttggaacta tgccgagtca tggatcagtt 1320
15 ggagcatcga ttacggcgat cgcagtcaat ccaacaccgt ctcttcaga acctatccca 1380
acatcacaac caacatcgaa atcagaatca tcttctatac tcgaaactgc acacgatgat 1440
cctttggaca cgtcgatacg tgctccagtg aaagacttgc atatgccgca tcgagcagtc 1500
20 aaggaacgaa tagccacgtt gcaaaatcac aaattcgca cgcttcgttc ccagagaata 1560
atcaatcagg aacaagaaga atatacgaaa gagaacaata tgtatgagca aatgagcaag 1620
25 tacaagcatc tacgacaagc acatcacaaa gagctccaac aatttgaaga acgatgtgca 1680
ttagatagag agcaactgcg tgtgaaaatg gatcgagaac tcgaacaatt gacaacgaca 1740
tactcgaaag aaaagatgag agtgaggtgt tcacagaata atgaactaga caaacggaaa 1800
30 aaagatatcg aagatgggga gaaaaagatg aaaaagacga aaaatagtca aaatcagcag 1860
cagatgaaac tgtattcagc gcaacaattg aaagaataca agtataacaa ggaggcacag 1920
35 aaaacacgat tacgaagtct gaacatgcct cgaagtactt atgagaacgc aatgaaagaa 1980
gtgaaagccg atctgaatcg agtgaaagat gcacgggaaa atgattttga cgagaagctt 2040
cgtgcagaac ttgaagatga aattgtaagg tatcgcaggc aacaactcag taatcttcat 2100
40 caattggaag aacaattgga tgatgaagac gtaaacgtgc aagaacgcca aatggacacg 2160
cgtcacggat tactgtcaaa gcagcatgaa atgacgcgcg atttggaaat acagcatctc 2220
45 aacgagcttc acgcatgaa aaaacgacat ttggagacac aacacgaggc ggaatcggca 2280
agtcaaaatg agtacacaca gaggcaacag gatgaattga gaaaaaagca tgcgatgcag 2340
tcaagacaac agccaagaga tttaaagatc caagaagcac aaattcgaaa acaataccga 2400
50 caagttgtga agactcagac tcgccaatth aagctctacc ttacacaaat ggtgcaagta 2460
gttccaaaag atgaacaaaa agagctcacg tctcgactaa aacaggatca aatgcaaaaa 2520
55 gtcgcacttc ttgcttcaca atacgaaagt caaatcaaaa aaatggttca ggataagaca 2580
gtgaagctcg agtcgtggca agaagatgaa caacgggttc ttagtgagaa gttggagaaa 2640

gaattggaag aattgattgc ttatcagaag aagacgagag ccacattaga agagcagatt 2700
 aaaaaggaac gtacggcact cgaagaacga attggcacac gacgtgcaat gcttgaacag 2760
 5 aagattattg aagaacgcga acaaattggga gaaatgcgtc gactaaagaa ggagcaaatac 2820
 cgtgatcgac acagtcaaga acgccatcgt ctcgagaatc atttcgtacg gacgggctcg 2880
 10 acgagcagaa gttctgggtg gatcgctcct ggtgttggga attcaagcag tattcagatg 2940
 gctatgtag 2949

15 <210> 2
 <211> 982
 <212> PRT
 20 <213> *Caenorhabditis elegans*
 <400> 2

25 Met Ala Pro Ala Val Leu Gln Lys Pro Gly Val Ile Lys Asp Pro Ser
 1 5 10 15
 Ile Ala Ala Leu Phe Ser Asn Lys Asp Pro Glu Gln Arg Tyr Gln Asp
 20 25 30
 30 Leu Arg Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Tyr
 35 40 45
 Asp Lys Lys Asn Glu Gln Thr Val Ala Ile Lys Lys Met Asn Phe Ser
 50 55 60
 Gly Lys Gln Ala Val Glu Lys Trp Asn Asp Ile Leu Lys Glu Val Ser
 65 70 75 80
 40 Phe Leu Asn Thr Val Val His Pro His Ile Val Asp Tyr Lys Ala Cys
 85 90 95
 Phe Leu Lys Asp Thr Thr Cys Trp Leu Val Met Glu Tyr Cys Ile Gly
 100 105 110
 45 Ser Ala Ala Asp Ile Val Asp Val Leu Arg Lys Gly Met Arg Glu Val
 115 120 125
 Glu Ile Ala Ala Ile Cys Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu
 130 135 140
 50 His Ser Leu Lys Arg Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu
 145 150 155 160
 55 Leu Ser Asp His Ala Ile Val Lys Leu Ala Asp Phe Gly Ser Ala Ser
 165 170 175

	Leu	Val	Asp	Pro	Ala	Gln	Thr	Phe	Ile	Gly	Thr	Pro	Phe	Phe	Met	Ala
				180					185						190	
5	Pro	Glu	Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	His	Tyr	Thr	Asp	Arg	Ala
			195					200					205			
	Asp	Ile	Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Arg
		210					215					220				
10	Pro	Pro	Leu	Phe	Ser	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala
	225					230					235					240
	Gln	Asn	Asp	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Asp	Thr	Ser	Glu	Gln	Pro
					245					250					255	
15	Glu	Trp	Ser	Leu	Glu	Phe	Val	Gln	Phe	Ile	Asp	Lys	Cys	Leu	Arg	Lys
				260					265						270	
	Pro	Ala	Glu	Glu	Arg	Met	Ser	Ala	Glu	Glu	Cys	Phe	Arg	His	Pro	Phe
20			275					280					285			
	Ile	Gln	Arg	Ser	Arg	Pro	Ser	Asp	Thr	Ile	Gln	Glu	Leu	Ile	Gln	Arg
		290					295					300				
25	Thr	Lys	Asn	Met	Val	Leu	Glu	Leu	Asp	Asn	Phe	Gln	Tyr	Lys	Lys	Met
	305					310					315					320
	Arg	Lys	Leu	Met	Tyr	Leu	Asp	Glu	Thr	Glu	Gly	Lys	Glu	Gly	Ser	Glu
					325					330					335	
30	Gly	Asn	Gly	Ala	Ser	Asp	Asp	Leu	Asp	Phe	His	Gly	Asn	Glu	Ala	Asn
				340					345					350		
	Ser	Ile	Gly	Arg	Ala	Gly	Asp	Ser	Ala	Ser	Ser	Arg	Ser	Ala	Ser	Leu
35			355					360					365			
	Thr	Ser	Phe	Arg	Ser	Met	Gln	Ser	Ser	Gly	Gly	Ala	Gly	Leu	Leu	Val
		370					375					380				
40	Ser	Thr	Asn	Thr	Thr	Gly	Ala	Met	Asp	Asn	Val	His	Gly	Ser	Ser	Gly
	385					390					395					400
	Tyr	Gly	Asn	Gly	Ser	Ser	Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Pro
					405					410					415	
45	Pro	Ile	Pro	Ser	Gln	Met	Leu	Ser	Ser	Thr	Ser	Thr	Ser	Gly	Val	Gly
				420					425					430		
	Thr	Met	Pro	Ser	His	Gly	Ser	Val	Gly	Ala	Ser	Ile	Thr	Ala	Ile	Ala
50			435					440					445			
	Val	Asn	Pro	Thr	Pro	Ser	Pro	Ser	Glu	Pro	Ile	Pro	Thr	Ser	Gln	Pro
		450					455					460				
55	Thr	Ser	Lys	Ser	Glu	Ser	Ser	Ser	Ile	Leu	Glu	Thr	Ala	His	Asp	Asp
	465					470					475					480

Pro Arg Asp Leu Lys Ile Gln Glu Ala Gln Ile Arg Lys Gln Tyr Arg
 785 790 795 800
 5 Gln Val Val Lys Thr Gln Thr Arg Gln Phe Lys Leu Tyr Leu Thr Gln
 805 810 815
 Met Val Gln Val Val Pro Lys Asp Glu Gln Lys Glu Leu Thr Ser Arg
 820 825 830
 10 Leu Lys Gln Asp Gln Met Gln Lys Val Ala Leu Leu Ala Ser Gln Tyr
 835 840 845
 Glu Ser Gln Ile Lys Lys Met Val Gln Asp Lys Thr Val Lys Leu Glu
 850 855 860
 15 Ser Trp Gln Glu Asp Glu Gln Arg Val Leu Ser Glu Lys Leu Glu Lys
 865 870 875 880
 Glu Leu Glu Glu Leu Ile Ala Tyr Gln Lys Lys Thr Arg Ala Thr Leu
 885 890 895
 20 Glu Glu Gln Ile Lys Lys Glu Arg Thr Ala Leu Glu Glu Arg Ile Gly
 900 905 910
 25 Thr Arg Arg Ala Met Leu Glu Gln Lys Ile Ile Glu Glu Arg Glu Gln
 915 920 925
 Met Gly Glu Met Arg Arg Leu Lys Lys Glu Gln Ile Arg Asp Arg His
 930 935 940
 30 Ser Gln Glu Arg His Arg Leu Glu Asn His Phe Val Arg Thr Gly Ser
 945 950 955 960
 Thr Ser Arg Ser Ser Gly Gly Ile Ala Pro Gly Val Gly Asn Ser Ser
 965 970 975
 35 Ser Ile Gln Met Ala Met
 980
 40 <210> 3
 <211> 4188
 45 <212> DNA
 <213> Homo sapiens
 <300>
 50 <308> genbank
 <309> 2002-10-04
 55 <313> (1) .. (4188)

<300>

<308> genbank NM_016281

5 <309> 2002-10-04

<313> (1)..(4188)

<400> 3

10 gccggggaac aagccacagg agagcgactc aggaacaagt gtgggagagg aagcggcggc 60
ggcggcgccg ggcccggggg tggtgacagc aggtctgagg ttgcatcata aatacaaagg 120
15 actgaagtta taaaagagaa aagagaagtt tgctgctaaa atgaatctga gcaatatgga 180
atattttgtg ccacacacaa aaagggtactg aagatttacc ccccaaaaaa aattgtcaat 240
gagaaataaa gctaactgat atcaaaaagc agagcctgct ctactggcca tcatgcgtaa 300
20 aggggtgctg aaggaccag agattgccga tctattctac aaagatgatc ctgaggaact 360
ttttattggt ttgcatgaaa ttggacatgg aagttttgga gcagtttatt ttgctacaaa 420
25 tgctcacacc aatgaggtgg tggcaattaa gaagatgtcc tatagtggga agcagaccca 480
tgagaaatgg caagatattc ttaaggaagt taaattttta cgacaattga agcatcctaa 540
tactattgag tacaaaggct gttacttgaa agaacacact gcttggttgg tgatggaata 600
30 ttgcttaggc tcagcctctg atttattaga agttcataaa aaaccacttc aggaagtgga 660
gatcgctgcc attactcatg gagccttgca tggactagcc tacctacatt ctcatgcatt 720
35 gattcatagg gatattaaag caggaaatat tcttctaaca gagccaggtc aggtaaaact 780
agctgatttt ggatctgctt caatggcttc tcctgccaac tccttcgtgg gcacacctta 840
ctggatggct ccagaggtga tcttagctat ggatgaagga cagtatgatg ggaaagttga 900
40 tatttggtca cttggcatca cttgtattga attggcggaa cggaagccgc cccttttcaa 960
catgaatgca atgagtgcct tatatcacat tgcccagaat gactcccaa cgttacagtc 1020
45 taatgaatgg acagactcct ttaggagatt tgttgattac tgcttgacaga aaatacctca 1080
ggaaaggcca acatcagcag aactattaag gcatgacttt gttcgacgag accggccact 1140
acgtgtcctc attgacctca tacagaggac aaaagatgca gttcgtgagc tagataacct 1200
50 acagtaccga aaaatgaaaa aaatactttt ccaagagaca cggaatggac ccttgaatga 1260
gtcacaggag gatgaggaag acagtgaaca tgggaaccagc ctgaacaggg aaatggacag 1320
55 cctgggcagc aaccattcca ttccaagcat gtccgtgagc acaggcagcc agagcagcag 1380
tgtgaacagc atgcaggaag tcatggacga gagcagttcc gaacttgtca tgatgcacga 1440

	tgacgaaagc acaatcaatt ccagctcctc cgtcgtgcat aagaaagatc atgtattcat	1500
	aagggatgag gcggggccacg gcgatcccag gcctgagccg cggcctaccc agtcagttca	1560
5	gagccaggcc ctccactacc ggaacagaga gcgctttgcc acgatcaaat cagcatcttt	1620
	ggttacacga cagatccatg agcatgagca ggagaacgag ttgcgggaac agatgtcagg	1680
10	ttataagcgg atgcggcgcc agcaccagaa gcagctgac gccctggaga acaagctgaa	1740
	ggctgagatg gacgagcacc gcctcaagct acagaaggag gtggagacgc atgccaacaa	1800
	ctcgtccatc gagctggaga agctggccaa gaagcaagtg gctatcatag aaaaggaggc	1860
15	aaaggtagct gcagcagatg agaagaagtt ccagcaacag atcttggccc agcagaagaa	1920
	agatttgaca actttcttag aaagtcagaa gaagcagtat aagatttgta aggaaaaaat	1980
20	aaaagaggaa atgaatgagg accatagcac acccaagaaa gagaagcaag agcggatctc	2040
	caaacataaa gagaacttgc agcacacaca ggctgaagag gaagcccacc ttctcactca	2100
	acagagactg tactacgaca aaaattgtcg tttcttcaag cggaaaataa tgatcaagcg	2160
25	gcacgaggtg gagcagcaga acattcggga ggaactaaat aaaaagagga cccagaagga	2220
	gatggagcat gccatgctaa tccggcacga cgagtccacc cgagagctag agtacaggca	2280
30	gctgcacacg ttacagaagc tacgcatgga tctgatccgt ttacagcacc agacggaact	2340
	ggaaaaccag ctggagtaca ataagaggcg agaaagagaa ctgcacagaa agcatgtcat	2400
	ggaacttcgg caacagccaa aaaacttaaa ggccatggaa atgcaaatta aaaaacagtt	2460
35	tcaggacact tgcaaagtac agaccaaaca gtataaagca ctcaagaatc accagttgga	2520
	agttactcca aagaatgagc acaaaacaat cttaaagaca ctgaaagatg agcagacaag	2580
40	aaaacttgcc attttggcag agcagtatga acagagtata aatgaaatga tggcctctca	2640
	agcgttacgg ctagatgagg ctcaagaagc agaatgccag gccttgaggc tacagctcca	2700
	gcaggaaatg gagctgctca acgcctacca gagcaaaatc aagatgcaaa cagaggcaca	2760
45	acatgaacgt gagctccaga agctagagca gagagtgtct ctgcgagag cacaccttga	2820
	gcagaagatt gaagaggagc tggctgccct tcagaaggaa cgcagcgaga gaataaagaa	2880
50	cctattggaa aggcaagagc gagagattga aacttttgac atggagagcc tcagaatggg	2940
	atttggaat ttggttacat tagattttcc taaggaggac tacagatgag attaaatttt	3000
	ttgccattta caaaaaaaaaa aaaaaaaaaa aaacagaaaa aaattcagac cctgcaaaac	3060
55	cacattcccc attttaacgg gcgttgctct cactctctct ctctcttact cttactgaca	3120

tcgtgtcggg ctagtgcctg tttattctta ctccatcagg ggcccccttc ctccccccgt 3180
gtcaactttc agtgtctggc aaaacctggc cgtctcttct attcacagta cacgtcacag 3240
5 tattgatgtg attcaaaatg tttcagtga aactttggag acagttttta caaaaccaat 3300
aaaccaacaa caaaaaaagt ggatgtatat tgctttaagc aatcactcat taccaccaat 3360
10 ctgtgaaagt aaagcaaaaa ataataataa taaatgccaa gggggagaga gacacaatat 3420
ccgcagcctt acaccttaac tagctgctgc attattttat tttattttat ttttttggtg 3480
tttattcatc aggaataaaaa aaaacaaagt tttattaaag attgaaaatt tgatacat 3540
15 tacagaaact aattgtgatg tacatatcag tggtgacata ttattacttt tttggggacg 3600
ggggtgggtg ggggtgaagag atcttgtgat tttagactgc tgcagagtta acttgtctca 3660
gcatatctga tgtatcataa tcatttctgc tgtgcagagg agggatacac ttagggggctc 3720
20 acagatccca gtagcacaat tgggctttgg caaatgggta ttttgtgtat agaggaattt 3780
aaggagaggt attacttatt ttcataattgt attttaactg tttctcggat caaatttttt 3840
25 aacttcttct tcgtgttctt cccacctcc ttccttttcc agttcagtat ttggagttca 3900
acactgtctc tcaatcagat catctggatc tttttcttta tctcccttcc ccttcctaag 3960
tcccatttct tggtcataaa tattgcatta ttcacacttt caaactgtgt attttcttac 4020
30 aataaaaaat gatgaaaaaa aaaaaggctt tacttctttt gcatgcactt taaaaacaaa 4080
acaaaacatt tttcaggttc caaggaagag catgataact gtcagagctt ttaattatat 4140
35 ttgtaaataa aagtgttcat cacaaaaaaa aaaaaaaaaa aaaaaaaaaa 4188

<210> 4

40 <211> 898

<212> PRT

45 <213> Homo sapiens

<300>

50 <308> Genbank NP_057365.2

<309> 2002-10-01

<313> (1) .. (898)

55 <400> 4

	Met	Arg	Lys	Gly	Val	Leu	Lys	Asp	Pro	Glu	Ile	Ala	Asp	Leu	Phe	Tyr	
	1				5					10					15		
5	Lys	Asp	Asp	Pro	Glu	Glu	Leu	Phe	Ile	Gly	Leu	His	Glu	Ile	Gly	His	
				20					25					30			
	Gly	Ser	Phe	Gly	Ala	Val	Tyr	Phe	Ala	Thr	Asn	Ala	His	Thr	Asn	Glu	
			35					40					45				
10	Val	Val	Ala	Ile	Lys	Lys	Met	Ser	Tyr	Ser	Gly	Lys	Gln	Thr	His	Glu	
		50					55					60					
	Lys	Trp	Gln	Asp	Ile	Leu	Lys	Glu	Val	Lys	Phe	Leu	Arg	Gln	Leu	Lys	
	65					70					75					80	
15	His	Pro	Asn	Thr	Ile	Glu	Tyr	Lys	Gly	Cys	Tyr	Leu	Lys	Glu	His	Thr	
					85					90					95		
	Ala	Trp	Leu	Val	Met	Glu	Tyr	Cys	Leu	Gly	Ser	Ala	Ser	Asp	Leu	Leu	
20				100					105					110			
	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	Glu	Val	Glu	Ile	Ala	Ala	Ile	Thr	
			115					120					125				
25	His	Gly	Ala	Leu	His	Gly	Leu	Ala	Tyr	Leu	His	Ser	His	Ala	Leu	Ile	
		130					135					140					
	His	Arg	Asp	Ile	Lys	Ala	Gly	Asn	Ile	Leu	Leu	Thr	Glu	Pro	Gly	Gln	
	145					150					155					160	
30	Val	Lys	Leu	Ala	Asp	Phe	Gly	Ser	Ala	Ser	Met	Ala	Ser	Pro	Ala	Asn	
					165					170					175		
	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val	Ile	Leu	Ala	
35				180					185					190			
	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	Lys	Val	Asp	Ile	Trp	Ser	Leu	Gly	
		195						200					205				
40	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Lys	Pro	Pro	Leu	Phe	Asn	Met	
		210					215					220					
	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala	Gln	Asn	Asp	Ser	Pro	Thr	
	225					230					235					240	
45	Leu	Gln	Ser	Asn	Glu	Trp	Thr	Asp	Ser	Phe	Arg	Arg	Phe	Val	Asp	Tyr	
					245					250					255		
	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Glu	Arg	Pro	Thr	Ser	Ala	Glu	Leu	Leu	
50				260					265					270			
	Arg	His	Asp	Phe	Val	Arg	Arg	Asp	Arg	Pro	Leu	Arg	Val	Leu	Ile	Asp	
			275					280					285				
55	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	Val	Arg	Glu	Leu	Asp	Asn	Leu	Gln	
		290					295					300					

	Tyr	Arg	Lys	Met	Lys	Lys	Ile	Leu	Phe	Gln	Glu	Thr	Arg	Asn	Gly	Pro	
	305					310					315					320	
5	Leu	Asn	Glu	Ser	Gln	Glu	Asp	Glu	Glu	Asp	Ser	Glu	His	Gly	Thr	Ser	
					325					330					335		
	Leu	Asn	Arg	Glu	Met	Asp	Ser	Leu	Gly	Ser	Asn	His	Ser	Ile	Pro	Ser	
				340					345					350			
10	Met	Ser	Val	Ser	Thr	Gly	Ser	Gln	Ser	Ser	Ser	Val	Asn	Ser	Met	Gln	
			355					360					365				
	Glu	Val	Met	Asp	Glu	Ser	Ser	Ser	Glu	Leu	Val	Met	Met	His	Asp	Asp	
		370					375					380					
15	Glu	Ser	Thr	Ile	Asn	Ser	Ser	Ser	Ser	Val	Val	His	Lys	Lys	Asp	His	
	385					390					395					400	
	Val	Phe	Ile	Arg	Asp	Glu	Ala	Gly	His	Gly	Asp	Pro	Arg	Pro	Glu	Pro	
20					405					410					415		
	Arg	Pro	Thr	Gln	Ser	Val	Gln	Ser	Gln	Ala	Leu	His	Tyr	Arg	Asn	Arg	
				420					425					430			
25	Glu	Arg	Phe	Ala	Thr	Ile	Lys	Ser	Ala	Ser	Leu	Val	Thr	Arg	Gln	Ile	
			435					440					445				
	His	Glu	His	Glu	Gln	Glu	Asn	Glu	Leu	Arg	Glu	Gln	Met	Ser	Gly	Tyr	
		450					455					460					
30	Lys	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Ile	Ala	Leu	Glu	Asn	
	465					470					475					480	
	Lys	Leu	Lys	Ala	Glu	Met	Asp	Glu	His	Arg	Leu	Lys	Leu	Gln	Lys	Glu	
35					485					490					495		
	Val	Glu	Thr	His	Ala	Asn	Asn	Ser	Ser	Ile	Glu	Leu	Glu	Lys	Leu	Ala	
				500					505					510			
40	Lys	Lys	Gln	Val	Ala	Ile	Ile	Glu	Lys	Glu	Ala	Lys	Val	Ala	Ala	Ala	
			515					520					525				
	Asp	Glu	Lys	Lys	Phe	Gln	Gln	Gln	Ile	Leu	Ala	Gln	Gln	Lys	Lys	Asp	
		530					535					540					
45	Leu	Thr	Thr	Phe	Leu	Glu	Ser	Gln	Lys	Lys	Gln	Tyr	Lys	Ile	Cys	Lys	
	545					550					555					560	
	Glu	Lys	Ile	Lys	Glu	Glu	Met	Asn	Glu	Asp	His	Ser	Thr	Pro	Lys	Lys	
50					565					570					575		
	Glu	Lys	Gln	Glu	Arg	Ile	Ser	Lys	His	Lys	Glu	Asn	Leu	Gln	His	Thr	
				580					585					590			
55	Gln	Ala	Glu	Glu	Glu	Ala	His	Leu	Leu	Thr	Gln	Gln	Arg	Leu	Tyr	Tyr	
			595					600					605				

Asp Lys Asn Cys Arg Phe Phe Lys Arg Lys Ile Met Ile Lys Arg His
 610 615 620
 5 Glu Val Glu Gln Gln Asn Ile Arg Glu Glu Leu Asn Lys Lys Arg Thr
 625 630 635 640
 Gln Lys Glu Met Glu His Ala Met Leu Ile Arg His Asp Glu Ser Thr
 645 650 655
 10 Arg Glu Leu Glu Tyr Arg Gln Leu His Thr Leu Gln Lys Leu Arg Met
 660 665 670
 Asp Leu Ile Arg Leu Gln His Gln Thr Glu Leu Glu Asn Gln Leu Glu
 675 680 685
 15 Tyr Asn Lys Arg Arg Glu Arg Glu Leu His Arg Lys His Val Met Glu
 690 695 700
 Leu Arg Gln Gln Pro Lys Asn Leu Lys Ala Met Glu Met Gln Ile Lys
 20 705 710 715 720
 Lys Gln Phe Gln Asp Thr Cys Lys Val Gln Thr Lys Gln Tyr Lys Ala
 725 730 735
 25 Leu Lys Asn His Gln Leu Glu Val Thr Pro Lys Asn Glu His Lys Thr
 740 745 750
 Ile Leu Lys Thr Leu Lys Asp Glu Gln Thr Arg Lys Leu Ala Ile Leu
 755 760 765
 30 Ala Glu Gln Tyr Glu Gln Ser Ile Asn Glu Met Met Ala Ser Gln Ala
 770 775 780
 Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln Ala Leu Arg Leu
 35 785 790 795 800
 Gln Leu Gln Gln Glu Met Glu Leu Leu Asn Ala Tyr Gln Ser Lys Ile
 805 810 815
 40 Lys Met Gln Thr Glu Ala Gln His Glu Arg Glu Leu Gln Lys Leu Glu
 820 825 830
 Gln Arg Val Ser Leu Arg Arg Ala His Leu Glu Gln Lys Ile Glu Glu
 835 840 845
 45 Glu Leu Ala Ala Leu Gln Lys Glu Arg Ser Glu Arg Ile Lys Asn Leu
 850 855 860
 Leu Glu Arg Gln Glu Arg Glu Ile Glu Thr Phe Asp Met Glu Ser Leu
 50 865 870 875 880
 Arg Met Gly Phe Gly Asn Leu Val Thr Leu Asp Phe Pro Lys Glu Asp
 885 890 895
 55 Tyr Arg

<210> 5
<211> 4971
5 <212> DNA
<213> Homo sapiens
10 <300>
<308> Genbank NM_016151.1
15 <309> 2002-11-05
<313> (1)..(4971)
20 <400> 5
aattcggcac gagctgagac ggagaagagg agaggcagag agggcgcgagg gaccgtcagc 60
agcaccttag ctacaatcgt tcagctattc tcggaagaga gaaggagagag ggaggaggcc 120
25 ggggcgggag tgggggctgt caccctcgga ccccggcgtg agaggggccc tgcggccgga 180
cgtcctcggg gtggggcccc agtcggtggc cgaagacctc cagctcaggc ccctgggtcc 240
caaatttcca ggctttgccc ctctccttt ctcagatacc cgggtaacag tcctcatagt 300
30 ccagatatcc gggactcggg tcccaacctc tctaaacctg ggtctctgtt tcatagattt 360
tcaaatatca ggttcaggcc cctgcgtgca ccagtatccg gggttcattc cccgggcgtt 420
35 tcaaatatcg gattcagttc ccatcccgtt cagatattcg gggttcagac cccacaatca 480
gaaatccgga attcggcagc tgcgcacctc gacgaggggg aggactggac cgcgagggtca 540
gattagggttgc taccacctc ccctccaggg gaggttccc gggcccgccc ctcaggaagg 600
40 gcgaaagccg aggaagaggt ggcaagggga aaggtctcct tgcccctctc cctgcttggc 660
agagccgctg gaggaccca ggcggaagcg gaggcgctgg ggcaccatag tgaccctac 720
45 caggccaggc cccactctca gggccccag gggccaccat gccagctggg ggccgggccc 780
ggagcctgaa ggaccagat gtggctgagc tcttcttcaa ggatgacca gaaaagctct 840
tctctgacct ccgggaaatt ggccatggca gctttggagc cgtatacttt gcccgggatg 900
50 tccggaatag tgagggtgtg gccatcaaga agatgtccta cagtgggaag cagtccaatg 960
agaaatggca agacatcatc aaggagggtgc ggttcttaca gaagctccgg catcccaaca 1020
55 ccattcagta ccggggctgt tacctgaggg agcacacggc ttggctggta atggagtatt 1080
gcctgggctc agcttctgac cttctagaag tgcacaagaa accccttcag gaggtagaga 1140

tgcgagctgt gacccacggg ggccttcagg gcctggcata tctgcactcc cacaacatga 1200
tccatagggg tgtgaaggct ggaaacatcc tgctgtcaga gccaggggta gtgaagctag 1260
5 gggacttttg ttctgcgtcc atcatggcac ctgccaaactc cttcgtgggc accccatact 1320
ggatggcacc cgaggatgatc ctggccatgg atgaggggca gtacgatggc aaagtggacg 1380
10 tctgggtcctt ggggataacc tgcacgcagc tggctgaacg gaaaccaccg ctctttaaca 1440
tgaatgcgat gagtgcctta taccacattg cacagaacga atccccgtg ctccagtcag 1500
gacactggtc tgagtacttc cggaattttg tcgactcctg tcttcagaaa atccctcaag 1560
15 acagaccaac ctacagaggtt ctctgaagc accgctttgt gctccgggag cggccaccca 1620
cagtcacatc ggacctgatc cagaggacca aggatgccgt gcgggagctg gacaacctgc 1680
20 agtaccgcaa gatgaagaag atcctgttcc aagaggcacc caacggccct ggtgccgagg 1740
ccccagagga ggaagaggag gccgagccct acatgcaccg ggccgggact ctgaccagcc 1800
tcgagagtag ccactcagtg ccagcatgt ccatcagcgc ctccagccag agcagctccg 1860
25 tcaacagcct agcagatgcc tcagacaacg aggaagagga ggaggaggag gaggaagagg 1920
aggaggagga agaaggccct gaagcccggg agatggccat gatgcaggag ggggagcaca 1980
30 cagtcacctc tcacagctcc attatccacc ggctgccggg ctctgacaac ctatatgatg 2040
accctacca gccagagata acccccagcc ctctccagcc gcctgcagcc ccagctccca 2100
cttccaccac ctcttccgcc cgccgccggg cctactgccg taaccgagac cactttgcca 2160
35 ccatccgaac cgctccctg gtcagccgtc agatccagga gcatgagcag gactctgcgc 2220
tgcgggagca gctgagcggc tataagcgga tgcgacgaca gcaccagaag cagctgctgg 2280
40 ccctggagtc acggctgagg ggtgaacggg aggagcacag tgcacggctg cagcgggagc 2340
ttgaggcgca gcgggctggc tttggggcag aggcagaaaa gctggcccgg cggcaccagg 2400
ccataggtga gaaggaggca cgagctgcc aggccgagga gcggaagttc cagcagcaca 2460
45 tccttgggca gcagaagaag gagctggctg ccctgctgga ggcacagaag cggacctaca 2520
aacttcgcaa ggaacagctg aaggaggagc tccaggagaa cccagcact cccaagcggg 2580
50 agaaggccga gtggctgctg cggcagaagg agcagctcca gcagtgccag gcggaggagg 2640
aagcagggtc gctgcggcgg cagcgccagt actttgagct gcagtgtcgc cagtacaagc 2700
gcaagatggt gctggctcgg cacagcctgg accaggacct gctgcgggag gacctgaaca 2760
55 agaagcagac ccagaaggac ttggagtgtg cactgctgct tcggcagcac gaggccacgc 2820

gggagctgga gctgcggcag ctccaggccg tgcagcgcac gcgggctgag ctcacccgcc 2880
 tgcagcacca gacggagctg ggcaaccagc tggagtacaa caagcggcgt gagcaagagt 2940
 5 tgcggcagaa gcatgcggcc cagggttcgcc agcagcccaa gagcctcaaa gtacgtgcag 3000
 gccagcgcgc cccgggcctt ccaactcccca ttcttggggc tctgggcccc cccaacacag 3060
 10 gcacccctat agaacagcag ccctgctcac ctggccagga ggagtcctg gaccaaagaa 3120
 tgcttggcga ggaggaggaa gcagttggag agagaaggat tctgggaaag gaagggggcca 3180
 ctttggagcc caagcagcag aggattctgg gggaagaatc aggagcccct agtcccagtc 3240
 15 cacaaaaaca tgggagcctg gttgatgagg aagtttgggg tctgcctgag gagatagagg 3300
 agcttagggg gccctccctt gtaccccagg agaggagcat tgttggccag gaggaggctg 3360
 20 ggacgtggag cttgtggggg aaggaggatg agagtcttct ggatgaggag tttgagcttg 3420
 gctgggtcca gggcccagca ctgactcccg tccctgagga ggaggaagaa gaggaagagg 3480
 gggctccgat tgggaccctt agggatcctg gagatggttg tccttcccc cactccctc 3540
 25 ctgaaccccc tccaacacac ctgaggccct gccctgccag ccagctccct ggactcctgt 3600
 cccatggcct cctggccggc ctctccttgg cagtggggtc ctctctggc ctctgcccc 3660
 30 tcctgctgct gctgctgctt ccattgctgg cagcccaggg tgggggtggc ctgcaggcag 3720
 cgctgctggc ccttgagggtg gggctgggtg gtctgggggc ctctacctg ctctttgta 3780
 cagccctgca cctgccctcc agtcttttcc tactcctggc ccagggtacc gactggggg 3840
 35 ccgtcctggg cctgagctgg cgccagggcc tcatgggtgt tcccctgggc cttggagctg 3900
 cctggctctt agcttggcca ggcctagctc tacctctggt ggctatggca gcggggggca 3960
 40 gatgggtgcg gcagcagggc ccccgggtgc gccggggcat atctcgactc tggttgcggg 4020
 ttctgctgcg cctgtcacc atggccttcc gggccctgca gggctgtggg gctgtgggg 4080
 accggggtct gtttgactg taccctaaaa ccaacaagga tggcttccgc agccgcctgc 4140
 45 ccgtccctgg gcccggcg cgtaatcccc gcaccacca acaccatta gctctgttgg 4200
 caagggtctg ggtcctgtgc aagggtgga actggcgtct ggcacgggcc agccagggtt 4260
 50 tagcatccca cttgcccccg tgggcatcc acacactggc cagctggggc ctgcttcggg 4320
 gtgaacggcc caccgaatc cccgggtac taccacgcag ccagcgccag ctagggcccc 4380
 ctgcctccca ccagccactg ccagggactc tagccgggcg gaggtcacgc acccgccagt 4440
 55 cccgggcctt gccccctgg aggtagctga ctccagccct tccagcccaa atctagagca 4500
 ttgagcactt tatctccac gactcagtga agtttctcca gtccctagtc ctctcttttc 4560

acccaccttc ctcagtttgc tcacttaccc caggcccagc ccttcggacc tctagacagg 4620
 cagcctcctc agctgtggag tccagcagtc actctgtgtt ctctgggcgc tcctccccta 4680
 5 agttattgct gttcgcccgc tgtgtgtgct catcctcacc ctcattgact caggcctggg 4740
 gccaggggtg gtggaggggtg ggaagagtca tgtttttttt ctctcttttg attttgtttt 4800
 10 tctgtctccc ttccaacctg tccccttccc ccacacaaaa aaagaaaaag acaaacacaa 4860
 ataaaatata tgagcggaac tgtgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4920
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 4971
 15

<210> 6

<211> 1235

20

<212> PRT

<213> Homo sapiens

25

<300>

<308> Genbank NP_057235.1

30

<309> 2002-11-05

<313> (1)..(1235)

35

<400> 6

Met Pro Ala Gly Gly Arg Ala Gly Ser Leu Lys Asp Pro Asp Val Ala
 1 5 10 15
 40 Glu Leu Phe Phe Lys Asp Asp Pro Glu Lys Leu Phe Ser Asp Leu Arg
 20 25 30
 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
 35 40 45
 45 Arg Asn Ser Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
 50 55 60
 50 Gln Ser Asn Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Arg Phe Leu
 65 70 75 80
 Gln Lys Leu Arg His Pro Asn Thr Ile Gln Tyr Arg Gly Cys Tyr Leu
 85 90 95
 55 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
 100 105 110

	Ser	Asp	Leu	Leu	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	Glu	Val	Glu	Ile	
			115					120					125				
5	Ala	Ala	Val	Thr	His	Gly	Ala	Leu	Gln	Gly	Leu	Ala	Tyr	Leu	His	Ser	
			130				135					140					
	His	Asn	Met	Ile	His	Arg	Asp	Val	Lys	Ala	Gly	Asn	Ile	Leu	Leu	Ser	
	145					150					155					160	
10	Glu	Pro	Gly	Leu	Val	Lys	Leu	Gly	Asp	Phe	Gly	Ser	Ala	Ser	Ile	Met	
					165					170					175		
	Ala	Pro	Ala	Asn	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	
				180					185					190			
15	Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	Lys	Val	Asp	Val	
			195					200					205				
	Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Lys	Pro	Pro	
20			210				215					220					
	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala	Gln	Asn	
	225					230					235					240	
25	Glu	Ser	Pro	Val	Leu	Gln	Ser	Gly	His	Trp	Ser	Glu	Tyr	Phe	Arg	Asn	
					245					250					255		
	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Asp	Arg	Pro	Thr	Ser	
				260					265					270			
30	Glu	Val	Leu	Leu	Lys	His	Arg	Phe	Val	Leu	Arg	Glu	Arg	Pro	Pro	Thr	
			275					280					285				
	Val	Ile	Met	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	Val	Arg	Glu	Leu	
35			290				295					300					
	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Ile	Leu	Phe	Gln	Glu	Ala	
	305					310					315					320	
40	Pro	Asn	Gly	Pro	Gly	Ala	Glu	Ala	Pro	Glu	Glu	Glu	Glu	Glu	Ala	Glu	
					325					330					335		
	Pro	Tyr	Met	His	Arg	Ala	Gly	Thr	Leu	Thr	Ser	Leu	Glu	Ser	Ser	His	
				340					345					350			
45	Ser	Val	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	Ser	Ser	Ser	Val	
			355					360					365				
	Asn	Ser	Leu	Ala	Asp	Ala	Ser	Asp	Asn	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
50			370				375					380					
	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Pro	Glu	Ala	Arg	Glu	Met	Ala	
	385					390					395					400	
55	Met	Met	Gln	Glu	Gly	Glu	His	Thr	Val	Thr	Ser	His	Ser	Ser	Ile	Ile	
					405					410					415		

	His	Arg	Leu	Pro	Gly	Ser	Asp	Asn	Leu	Tyr	Asp	Asp	Pro	Tyr	Gln	Pro	
				420					425					430			
5	Glu	Ile	Thr	Pro	Ser	Pro	Leu	Gln	Pro	Pro	Ala	Ala	Pro	Ala	Pro	Thr	
			435					440					445				
	Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Ala	Tyr	Cys	Arg	Asn	Arg	Asp	
			450				455					460					
10	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val	Ser	Arg	Gln	Ile	Gln	
	465					470					475					480	
	Glu	His	Glu	Gln	Asp	Ser	Ala	Leu	Arg	Glu	Gln	Leu	Ser	Gly	Tyr	Lys	
					485					490					495		
15	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Leu	Ala	Leu	Glu	Ser	Arg	
				500					505					510			
	Leu	Arg	Gly	Glu	Arg	Glu	Glu	His	Ser	Ala	Arg	Leu	Gln	Arg	Glu	Leu	
20			515					520					525				
	Glu	Ala	Gln	Arg	Ala	Gly	Phe	Gly	Ala	Glu	Ala	Glu	Lys	Leu	Ala	Arg	
		530				535						540					
25	Arg	His	Gln	Ala	Ile	Gly	Glu	Lys	Glu	Ala	Arg	Ala	Ala	Gln	Ala	Glu	
	545					550					555					560	
	Glu	Arg	Lys	Phe	Gln	Gln	His	Ile	Leu	Gly	Gln	Gln	Lys	Lys	Glu	Leu	
				565						570					575		
30	Ala	Ala	Leu	Leu	Glu	Ala	Gln	Lys	Arg	Thr	Tyr	Lys	Leu	Arg	Lys	Glu	
			580						585					590			
	Gln	Leu	Lys	Glu	Glu	Leu	Gln	Glu	Asn	Pro	Ser	Thr	Pro	Lys	Arg	Glu	
35			595					600					605				
	Lys	Ala	Glu	Trp	Leu	Leu	Arg	Gln	Lys	Glu	Gln	Leu	Gln	Gln	Cys	Gln	
		610					615					620					
40	Ala	Glu	Glu	Glu	Ala	Gly	Leu	Leu	Arg	Arg	Gln	Arg	Gln	Tyr	Phe	Glu	
	625					630					635					640	
	Leu	Gln	Cys	Arg	Gln	Tyr	Lys	Arg	Lys	Met	Leu	Leu	Ala	Arg	His	Ser	
				645						650					655		
45	Leu	Asp	Gln	Asp	Leu	Leu	Arg	Glu	Asp	Leu	Asn	Lys	Lys	Gln	Thr	Gln	
			660						665					670			
	Lys	Asp	Leu	Glu	Cys	Ala	Leu	Leu	Leu	Arg	Gln	His	Glu	Ala	Thr	Arg	
50			675					680					685				
	Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr	Arg	Ala	Glu	
		690					695					700					
55	Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln	Leu	Glu	Tyr	
	705					710					715					720	

	Asn	Lys	Arg	Arg	Glu	Gln	Glu	Leu	Arg	Gln	Lys	His	Ala	Ala	Gln	Val	
					725					730					735		
5	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Val	Arg	Ala	Gly	Gln	Arg	Pro	Pro	
				740					745					750			
	Gly	Leu	Pro	Leu	Pro	Ile	Pro	Gly	Ala	Leu	Gly	Pro	Pro	Asn	Thr	Gly	
			755					760					765				
10	Thr	Pro	Ile	Glu	Gln	Gln	Pro	Cys	Ser	Pro	Gly	Gln	Glu	Ala	Val	Leu	
		770					775					780					
	Asp	Gln	Arg	Met	Leu	Gly	Glu	Glu	Glu	Glu	Ala	Val	Gly	Glu	Arg	Arg	
	785					790					795					800	
15	Ile	Leu	Gly	Lys	Glu	Gly	Ala	Thr	Leu	Glu	Pro	Lys	Gln	Gln	Arg	Ile	
					805					810					815		
	Leu	Gly	Glu	Glu	Ser	Gly	Ala	Pro	Ser	Pro	Ser	Pro	Gln	Lys	His	Gly	
20					820				825					830			
	Ser	Leu	Val	Asp	Glu	Glu	Val	Trp	Gly	Leu	Pro	Glu	Glu	Ile	Glu	Glu	
			835					840					845				
25	Leu	Arg	Val	Pro	Ser	Leu	Val	Pro	Gln	Glu	Arg	Ser	Ile	Val	Gly	Gln	
		850					855					860					
	Glu	Glu	Ala	Gly	Thr	Trp	Ser	Leu	Trp	Gly	Lys	Glu	Asp	Glu	Ser	Leu	
	865					870					875					880	
30	Leu	Asp	Glu	Glu	Phe	Glu	Leu	Gly	Trp	Val	Gln	Gly	Pro	Ala	Leu	Thr	
					885					890					895		
	Pro	Val	Pro	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Pro	Ile	Gly	
35				900					905					910			
	Thr	Pro	Arg	Asp	Pro	Gly	Asp	Gly	Cys	Pro	Ser	Pro	Asp	Ile	Pro	Pro	
			915					920					925				
40	Glu	Pro	Pro	Pro	Thr	His	Leu	Arg	Pro	Cys	Pro	Ala	Ser	Gln	Leu	Pro	
		930					935					940					
	Gly	Leu	Leu	Ser	His	Gly	Leu	Leu	Ala	Gly	Leu	Ser	Phe	Ala	Val	Gly	
	945					950					955					960	
45	Ser	Ser	Ser	Gly	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Leu	
					965				970						975		
	Leu	Ala	Ala	Gln	Gly	Gly	Gly	Gly	Leu	Gln	Ala	Ala	Leu	Leu	Ala	Leu	
50				980					985					990			
	Glu	Val	Gly	Leu	Val	Gly	Leu	Gly	Ala	Ser	Tyr	Leu	Leu	Leu	Cys	Thr	
			995					1000					1005				
55	Ala	Leu	His	Leu	Pro	Ser	Ser	Leu	Phe	Leu	Leu	Leu	Ala	Gln	Gly		
		1010					1015						1020				

[illegible]

<308> Genbank NM_004783

<309> 2000-11-01

5 <313> (1)..(4242)

<400> 7

10	agaatttcaa atatcaggtt caggccccctg cgtgcaccag tatccggggt tcattccccg	60
	ggcgttcaaa tatcggattc agtctccatc ccgttcagat attcgggggt cagacccccac	120
	aatcagaaat ccggaattcg gcagctgtcg ccctcgacga gggggaggac tggaccgcga	180
15	ggtcagatta gggtgtcacc ccctccccctc caggggaggc ttcccggggc cggcccctcag	240
	gaagggcgaa agccgaggaa gaggtggcaa ggggaaaggc ctccctgccc ctctccctgc	300
	ttggcagagc cgctggagga cccagggcgg aagcggaggc gctggggcac catagtgacc	360
20	cctaccaggc caggccccac tctcagggcc ccagggggcc accatgccag ctggggggccg	420
	ggccgggagc ctgaaggacc cagatgtggc tgagctcttc ttcaaggatg acccagaaaa	480
25	gctcttctct gacctccggg aaattggcca tggcagcttt ggagccgtat actttgcccg	540
	ggatgtccgg aatagtgagg tgggtggcat caagaagatg tcctacagtg ggaagcagtc	600
	caatgagaaa tggcaagaca tcatcaagga ggtgcggttc ttacagaagc tccggcatcc	660
30	caacaccatt cagtaccggg gctgttacct gagggagcac acggcttggc tggtaatgga	720
	gtattgcctg ggctcagctt ctgaccttct agaagtgcac aagaaacccc ttcaggaggt	780
35	agagatcgca gctgtgaccc acggggcgct tcagggcctg gcatatctgc actcccacaa	840
	catgatccat agggatgtga aggctggaaa catcctgctg tcagagccag ggtagtgaa	900
	gctaggggac tttgggtctg cgtccatcat ggcacctgcc aactccttcg tgggcacccc	960
40	atactggatg gcacccgagg tgatcctggc catggatgag gggcagtagc atggcaaagt	1020
	ggacgtctgg tccttgggga taacctgcat cgagctggct gaacggaaac caccgctctt	1080
45	taacatgaat gcgatgagt ccttatacca cattgcacag aacgaatccc ccgtgctcca	1140
	gtcaggacac tgggtctgagt acttccggaa ttttgtcgac tcctgtcttc agaaaatccc	1200
	tcaagacaga ccaacctcag aggttctcct gaagcaccgc tttgtgctcc gggagcggcc	1260
50	accacagtc atcatggacc tgatccagag gaccaaggat gccgtgcggg agctggacaa	1320
	cctgcagtac cgcaagatga agaagatcct gttccaagag gcaccaacg gccctggtgc	1380
55	cgaggcccca gaggaggaag aggaggccga gccctacatg caccggggccg ggactctgac	1440
	cagcctcgag agtagccact cagtgccag catgtccatc agcgcctcca gccagagcag	1500

	ctccgtcaac	agcctagcag	atgcctcaga	caacgaggaa	gaggaggagg	aggaggagga	1560
5	agaggaggag	gaggaagaag	gccctgaagc	ccgggagatg	gccatgatgc	aggaggggga	1620
	gcacacagtc	acctctcaca	gctccattat	ccaccggctg	ccgggctctg	acaacctata	1680
	tgatgacccc	taccagccag	agataacccc	cagccctctc	cagccgcctg	cagccccagc	1740
10	tccccattcc	accacctctt	ctgcccgcgc	ccggggcctac	tgccgtaacc	gagaccactt	1800
	tgccaccatc	cgaaccgcct	ccctggtcag	ccgtcagatc	caggagcatg	agcaggactc	1860
15	tgcgctgcgg	gagcagctga	gcggctataa	gcggatgcga	cgacagcacc	agaagcagct	1920
	gctggccctg	gagtcacggc	tgaggggtga	acgggaggag	cacagtgcac	ggctgcagcg	1980
	ggagcttgag	gcgcagcggg	ctggctttgg	ggcagaggca	gaaaagctgg	cccggcggca	2040
20	ccaggccata	ggtgagaagg	aggcacgagc	tgcccaggcc	gaggagcggg	agttccagca	2100
	gcacatcctt	gggcagcaga	agaaggagct	ggctgccctg	ctggaggcac	agaagcggac	2160
25	ctacaaaactt	cgcaaggaac	agctgaagga	ggagctccag	gagaacccca	gcactcccaa	2220
	gcggggagaag	gccgagtggc	tgctgcggca	gaaggagcag	ctccagcagt	gccaggcggg	2280
	ggaggaagca	gggctgctgc	ggcggcagcg	ccagtacttt	gagctgcagt	gtcgccagta	2340
30	caagcgcaag	atgttgctgg	ctcggcacag	cctggaccag	gacctgctgc	gggaggacct	2400
	gaacaagaag	cagaccacaga	aggacttgga	gtgtgcactg	ctgcttcggc	agcacgaggc	2460
35	cacgcgggag	ctggagctgc	ggcagctcca	ggccgtgcag	cgcacgcggg	ctgagctcac	2520
	ccgcctgcag	caccagacgg	agctgggcaa	ccagctggag	tacaacaagc	ggcgtgagca	2580
	agagttgcgg	cagaagcatg	cggcccaggt	tcgccagcag	cccaagagcc	tcaaactctaa	2640
40	ggagctgcag	atcaagaagc	agttccagga	gacgtgtaag	atccagactc	ggcagtacaa	2700
	ggctctgcga	gcacacttgc	tgagagaccac	gccccaaagct	cagcacaaga	gcctccttaa	2760
45	gcggctcaag	gaagagcaga	cccgcgaagct	ggcgatcttg	gcggagcagt	atgaccagtc	2820
	catctcagag	atgctcagct	cacaggcgct	gcggcttgat	gagacccagg	aggcagagtt	2880
	ccaggccctt	cggcagcagc	ttcaacagga	gctggagctg	ctcaacgctt	accagagcaa	2940
50	gatcaagatc	cgcacagaga	gccagcacga	gaggagagctg	cgggagctgg	agcagagggg	3000
	cgcgctgcgg	cgggcactgc	tgagagcagc	ggtggaagag	gagctgctgg	ccctgcagac	3060
55	aggacgctcc	gagcgaatcc	gcagtctgct	tgagcggcag	gcccgtgaga	tcgaggcctt	3120
	cgatgcggaa	agcatgaggc	tgggcttctc	cagcatggct	ctgggggggca	tcccggctga	3180

agctgctgcc cagggctatc ctgctccacc ccctgccccca gcctggccct cccgtcccgt 3240
tccccgttct ggggcacact ggagccatgg ccctcctcca ccaggcatgc cccctccagc 3300
5 ctggcgctcag ccgtctctgc tggctcccc aggcccccca aactggctgg ggccccccac 3360
acaaagtggg acaccccgctg gcggagccct gctgctgcta agaaacagcc cccagcccct 3420
10 gcggcgggca gcctcggggg gcagtggcag tgagaatgtg ggccccctg ctgccgcggt 3480
gcccggggcc ctgagccgca gcaccagtgt cgcttccca atcctcaatg gttcttccca 3540
cttctattcc tgaggtgcag cggggaggag cagatgagct gggcagggca ggggtgggtg 3600
15 gagcctgacc ctggagggca ctgagctgga ggcccctgca agggtagggg acaagatgta 3660
ggctccagct cccctcagac ctctcatct catgagcttc ttggggctgg ccagtggccc 3720
agggccagct tggcgataga tgcctcaagg ctgcctggga gcccgcctc cctaccatgg 3780
20 tgccaggggt ctccctccgc cacctaggaa aggagggaga tgtgcgtgtc aaatattcat 3840
ctagtccctt gggggagggg aagggtgggt ctagacatac tatattcaga gaactatact 3900
25 accctcacag tgaggccctc agacctgcca cagggcagag caggtctggg gcctgaggca 3960
gggagaatga gaggccacct tactggcagg aaggatcagg atggggctctt ggggtcagga 4020
tgctgggtc tcttcccgta actgtctgac gtcctgtgcc gtcttgcct ttatcttttt 4080
30 tttttttttt taattgggat cagggtctggg gcggggaaac aagggaagga ccttggaagg 4140
ggctgctccc aggcctgggg ggcagctcgt ggagcccctc tcagctgtgg ggctggcaca 4200
35 gagccccagg caagctttta ataaactgtt ggttattcta ac 4242

<210> 8

40 <211> 1049

<212> PRT

45 <213> Homo sapiens

<300>

50 <308> Genbank NP_004774.1

<309> 2000-11-01

<313> (1) .. (1049)

55

<400> 8

	Met	Pro	Ala	Gly	Gly	Arg	Ala	Gly	Ser	Leu	Lys	Asp	Pro	Asp	Val	Ala	
	1				5					10					15		
5	Glu	Leu	Phe	Phe	Lys	Asp	Asp	Pro	Glu	Lys	Leu	Phe	Ser	Asp	Leu	Arg	
				20					25					30			
	Glu	Ile	Gly	His	Gly	Ser	Phe	Gly	Ala	Val	Tyr	Phe	Ala	Arg	Asp	Val	
			35					40					45				
10	Arg	Asn	Ser	Glu	Val	Val	Ala	Ile	Lys	Lys	Met	Ser	Tyr	Ser	Gly	Lys	
		50					55					60					
	Gln	Ser	Asn	Glu	Lys	Trp	Gln	Asp	Ile	Ile	Lys	Glu	Val	Arg	Phe	Leu	
	65					70					75					80	
15	Gln	Lys	Leu	Arg	His	Pro	Asn	Thr	Ile	Gln	Tyr	Arg	Gly	Cys	Tyr	Leu	
					85					90					95		
	Arg	Glu	His	Thr	Ala	Trp	Leu	Val	Met	Glu	Tyr	Cys	Leu	Gly	Ser	Ala	
20				100					105					110			
	Ser	Asp	Leu	Leu	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	Glu	Val	Glu	Ile	
			115					120					125				
25	Ala	Ala	Val	Thr	His	Gly	Ala	Leu	Gln	Gly	Leu	Ala	Tyr	Leu	His	Ser	
		130					135					140					
	His	Asn	Met	Ile	His	Arg	Asp	Val	Lys	Ala	Gly	Asn	Ile	Leu	Leu	Ser	
	145					150					155					160	
30	Glu	Pro	Gly	Leu	Val	Lys	Leu	Gly	Asp	Phe	Gly	Ser	Ala	Ser	Ile	Met	
				165						170					175		
	Ala	Pro	Ala	Asn	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	
35				180					185					190			
	Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	Lys	Val	Asp	Val	
			195					200					205				
40	Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Lys	Pro	Pro	
		210					215					220					
	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala	Gln	Asn	
	225					230					235					240	
45	Glu	Ser	Pro	Val	Leu	Gln	Ser	Gly	His	Trp	Ser	Glu	Tyr	Phe	Arg	Asn	
				245						250					255		
	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Asp	Arg	Pro	Thr	Ser	
50				260					265					270			
	Glu	Val	Leu	Leu	Lys	His	Arg	Phe	Val	Leu	Arg	Glu	Arg	Pro	Pro	Thr	
			275					280					285				
55	Val	Ile	Met	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	Val	Arg	Glu	Leu	
		290					295					300					

	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Ile	Leu	Phe	Gln	Glu	Ala	
	305					310					315					320	
5	Pro	Asn	Gly	Pro	Gly	Ala	Glu	Ala	Pro	Glu	Glu	Glu	Glu	Glu	Ala	Glu	
					325					330					335		
	Pro	Tyr	Met	His	Arg	Ala	Gly	Thr	Leu	Thr	Ser	Leu	Glu	Ser	Ser	His	
				340					345					350			
10	Ser	Val	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	Ser	Ser	Ser	Val	
			355					360					365				
	Asn	Ser	Leu	Ala	Asp	Ala	Ser	Asp	Asn	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
15		370					375					380					
	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Pro	Glu	Ala	Arg	Glu	Met	Ala	
	385					390					395					400	
20	Met	Met	Gln	Glu	Gly	Glu	His	Thr	Val	Thr	Ser	His	Ser	Ser	Ile	Ile	
					405					410					415		
	His	Arg	Leu	Pro	Gly	Ser	Asp	Asn	Leu	Tyr	Asp	Asp	Pro	Tyr	Gln	Pro	
				420					425					430			
25	Glu	Ile	Thr	Pro	Ser	Pro	Leu	Gln	Pro	Pro	Ala	Ala	Pro	Ala	Pro	Thr	
			435					440					445				
	Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Ala	Tyr	Cys	Arg	Asn	Arg	Asp	
30		450					455					460					
	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val	Ser	Arg	Gln	Ile	Gln	
	465					470					475					480	
35	Glu	His	Glu	Gln	Asp	Ser	Ala	Leu	Arg	Glu	Gln	Leu	Ser	Gly	Tyr	Lys	
					485					490					495		
	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Leu	Ala	Leu	Glu	Ser	Arg	
				500				505						510			
40	Leu	Arg	Gly	Glu	Arg	Glu	Glu	His	Ser	Ala	Arg	Leu	Gln	Arg	Glu	Leu	
			515					520					525				
	Glu	Ala	Gln	Arg	Ala	Gly	Phe	Gly	Ala	Glu	Ala	Glu	Lys	Leu	Ala	Arg	
45		530				535						540					
	Arg	His	Gln	Ala	Ile	Gly	Glu	Lys	Glu	Ala	Arg	Ala	Ala	Gln	Ala	Glu	
	545					550				555						560	
50	Glu	Arg	Lys	Phe	Gln	Gln	His	Ile	Leu	Gly	Gln	Gln	Lys	Lys	Glu	Leu	
					565					570					575		
	Ala	Ala	Leu	Leu	Glu	Ala	Gln	Lys	Arg	Thr	Tyr	Lys	Leu	Arg	Lys	Glu	
				580				585					590				
55	Gln	Leu	Lys	Glu	Glu	Leu	Gln	Glu	Asn	Pro	Ser	Thr	Pro	Lys	Arg	Glu	
			595					600					605				

	Lys	Ala	Glu	Trp	Leu	Leu	Arg	Gln	Lys	Glu	Gln	Leu	Gln	Gln	Cys	Gln	
	610						615					620					
5	Ala	Glu	Glu	Glu	Ala	Gly	Leu	Leu	Arg	Arg	Gln	Arg	Gln	Tyr	Phe	Glu	
	625					630					635					640	
	Leu	Gln	Cys	Arg	Gln	Tyr	Lys	Arg	Lys	Met	Leu	Leu	Ala	Arg	His	Ser	
					645					650					655		
10	Leu	Asp	Gln	Asp	Leu	Leu	Arg	Glu	Asp	Leu	Asn	Lys	Lys	Gln	Thr	Gln	
				660					665					670			
	Lys	Asp	Leu	Glu	Cys	Ala	Leu	Leu	Leu	Arg	Gln	His	Glu	Ala	Thr	Arg	
				675				680					685				
15	Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr	Arg	Ala	Glu	
		690					695					700					
	Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln	Leu	Glu	Tyr	
20		705				710					715					720	
	Asn	Lys	Arg	Arg	Glu	Gln	Glu	Leu	Arg	Gln	Lys	His	Ala	Ala	Gln	Val	
					725					730					735		
25	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Ser	Lys	Glu	Leu	Gln	Ile	Lys	Lys	
				740					745					750			
	Gln	Phe	Gln	Glu	Thr	Cys	Lys	Ile	Gln	Thr	Arg	Gln	Tyr	Lys	Ala	Leu	
			755					760					765				
30	Arg	Ala	His	Leu	Leu	Glu	Thr	Thr	Pro	Lys	Ala	Gln	His	Lys	Ser	Leu	
		770					775					780					
	Leu	Lys	Arg	Leu	Lys	Glu	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ile	Leu	Ala	
35		785				790				795						800	
	Glu	Gln	Tyr	Asp	Gln	Ser	Ile	Ser	Glu	Met	Leu	Ser	Ser	Gln	Ala	Leu	
					805					810					815		
40	Arg	Leu	Asp	Glu	Thr	Gln	Glu	Ala	Glu	Phe	Gln	Ala	Leu	Arg	Gln	Gln	
				820					825					830			
	Leu	Gln	Gln	Glu	Leu	Glu	Leu	Leu	Asn	Ala	Tyr	Gln	Ser	Lys	Ile	Lys	
			835				840					845					
45	Ile	Arg	Thr	Glu	Ser	Gln	His	Glu	Arg	Glu	Leu	Arg	Glu	Leu	Glu	Gln	
		850					855					860					
	Arg	Val	Ala	Leu	Arg	Arg	Ala	Leu	Leu	Glu	Gln	Arg	Val	Glu	Glu	Glu	
50		865				870					875					880	
	Leu	Leu	Ala	Leu	Gln	Thr	Gly	Arg	Ser	Glu	Arg	Ile	Arg	Ser	Leu	Leu	
					885					890					895		
55	Glu	Arg	Gln	Ala	Arg	Glu	Ile	Glu	Ala	Phe	Asp	Ala	Glu	Ser	Met	Arg	
				900					905					910			

Leu Gly Phe Ser Ser Met Ala Leu Gly Gly Ile Pro Ala Glu Ala Ala
915 920 925

5 Ala Gln Gly Tyr Pro Ala Pro Pro Pro Ala Pro Ala Trp Pro Ser Arg
930 935 940

Pro Val Pro Arg Ser Gly Ala His Trp Ser His Gly Pro Pro Pro Pro
945 950 955 960

10 Gly Met Pro Pro Pro Ala Trp Arg Gln Pro Ser Leu Leu Ala Pro Pro
965 970 975

Gly Pro Pro Asn Trp Leu Gly Pro Pro Thr Gln Ser Gly Thr Pro Arg
980 985 990

15 Gly Gly Ala Leu Leu Leu Leu Arg Asn Ser Pro Gln Pro Leu Arg Arg
995 1000 1005

20 Ala Ala Ser Gly Gly Ser Gly Ser Glu Asn Val Gly Pro Pro Ala
1010 1015 1020

Ala Ala Val Pro Gly Pro Leu Ser Arg Ser Thr Ser Val Ala Ser
1025 1030 1035

25 His Ile Leu Asn Gly Ser Ser His Phe Tyr Ser
1040 1045

<210> 9

30 <211> 3285

<212> DNA

35 <213> Homo sapiens

<220>

40 <221> misc_feature

<222> (3245)..(3245)

<223> a, t, c or g

45 <220>

<221> misc_feature

50 <222> (3263)..(3263)

<223> a, t, c or g

55 <220>

<221> misc_feature
 <222> (3278)..(3278)
 5 <223> a, t, c or g

 <220>
 10 <221> misc_feature
 <222> (72)..(72)
 <223> a, t, c or g
 15
 <300>
 <308> EMBL AY049015
 20 <309> 2001-10-15
 <313> (1)..(3285)
 25
 <400> 9
 caacggattt catttcatac agatgaacca aggatcgga tagcagtata aaattagaat 60
 caagacagct gnetgccaag caggatgcc aactaaca gagcaggcag cctgaaggac 120
 30 cctgaaattg cagagctctt cttcaaagaa gatccagaga agctcttcac agatctcaga 180
 gaaattggcc atggaagctt tggagcagt tattttgcac gagatgtgcg taccaatgaa 240
 35 gtggtggcca tcaagaaaat gtcttatagt ggaaagcagt ctactgagaa atggcaggat 300
 attattaagg aagtcaagtt tctacaaaga ataaaacatc ccaacagtat agaatacaaa 360
 ggctgttatt tacgtgaaca cacagcatgg cttgtaatgg aatattgttt aggatctgct 420
 40 tcggatttac tagaagttca caaaaagcca ttacaagaag tggaaatagc agcaattaca 480
 catggtgctc ttcagggatt agcctactta cattctcata ctatgattca tagagatatc 540
 45 aaagcaggaa atatccttct gacagaacca ggccaggatga aacttgctga ctttggctct 600
 gcttccatgg catcacctgc caattccttt gtgggaacgc cgtattggat ggccccagaa 660
 gtaatttttag ccatggatga aggacaatat gatggcaaag tagatgtgtg gtctcttgga 720
 50 ataacatgta ttgaactagc ggaaaggaag cctcctttat ttaatatgaa tgcaatgagt 780
 gccttatatc acatagccca aaatgaatcc cctacactac agtctaata atggtctgat 840
 55 tattttcgca actttgtaga ttcttgctc cagaaaatcc ctcaagatcg acctacatca 900
 gaggaacttt taaagcacat atttgttctt cgggagcgcc ctgaaaccgt gttaatagat 960

5 ctcattcaga ggacaaagga tgcagtaaga gagctggaca atctgcagta tcgaaagatg 1020
 aagaaactcc ttttccagga ggcacataat ggaccagcag tagaagcaca ggaagaagaa 1080
 gaggaacaag atcatgggtgt tggccggaca ggaacagtta atagtgttgg aagtaatcaa 1140
 tccattccca gcatgtccat cagtgccagc agccaaagca gtagtggttaa cagtcttcca 1200
 10 gatgtctcag atgacaagag tgagctagac atgatggagg gagaccacac agtgatgtct 1260
 aacagttctg ttatccattt aaaaccagag gaagaaaatt acagagaaga gggagatcct 1320
 agaacaagag catcagatcc acaatctcca cccaagtat ctcgtcaca atcacactat 1380
 15 cgtaatcgag aacactttgc tactatacgg acagcatcac tggttacgag gcaaatgcaa 1440
 gaacatgagc aggactctga gcttagagaa caaatgtctg gctataagcg aatgaggcga 1500
 20 caacatcaaa agcaactgat gactctggaa aacaagctaa aggctgagat ggatgaacat 1560
 cgcttcagat tagacaaaga tcttgaaact cagcgtaca attttgctgc agaaatggag 1620
 aaacttatca agaaacacca ggctgctatg gagaaagagg cttaaagtat gtccaatgaa 1680
 25 gagaaaaaat ttcagcaaca tattcaggcc caacagaaga aagaactgaa tagttttctc 1740
 gagtcccaga aaagagagta taaacttcga aaagagcagc ttaaagagga gctaaatgaa 1800
 30 aaccagagta cccccaaaa agaaaaacag gagtggcttt caaagcagaa ggagaatata 1860
 cagcatttcc aagcagaaga agaagctaac cttcttcgac gtcaaagaca atacctagag 1920
 ctggaatgcc gtcgcttcaa gagaagaatg ttacttgggc gtcataactt agagcaggac 1980
 35 cttgtcaggg aggagttaaa caaaagacag actcagaagg acttagagca tgccatgcta 2040
 ctccgacagc atgaatctat gcaagaactg gagttccgcc acctcaacac aattcagaag 2100
 40 atgcgctgtg agttgatcag attacagcat caaactgagc tcactaacca gctggaatat 2160
 aataagcgaa gagaacgaga actaagacga aagcatgtca tggaagttcg acaacagcct 2220
 aagagtttga agtctaaaga actccaaata aaaaagcagt ttcaggatac ctgcaaaatc 2280
 45 caaaccagac agtacaagc attaagaaat cacctgctgg agactacacc aaagagttag 2340
 cacaaagctg ttctgaaacg gctcaaggag gaacagaccc ggaaattagc tatcttggct 2400
 50 gagcagtatg atcacagcat taatgaaatg ctctccacac aagccctgcg tttggatgaa 2460
 gcacaggaag cagagtcca ggttttgaag atgcagctgc agcaggaact ggagctgttg 2520
 aatgcgtatc agagcaaaat caagatgcaa gctgaggcac aacatgatcg agagcttcgc 2580
 55 gagcttgaac agagggtctc cctccggagg gcactcttag aacaaaagat tgaagaagag 2640

```

atgttggctt tgcagaatga gcgcacagaa cgaatacgaa gcctgttgga acgtcaagcc 2700
agagagattg aagcttttga ctctgaaagc atgagactag gtttttagtaa tatgggtgctt 2760
5 tctaattctct cccctgaggc attcagccac agctacccgg gagcttctgg ttggtcacac 2820
aaccctactg ggggtccagg acctcactgg ggatcatcca tgggtggccc accacaagct 2880
10 tggggccatc caatgcaagg tggaccccag ccatgggggtc acccttcagg gccaatgcaa 2940
ggggtacctc gaggtagcag tatgggagtc cgcaatagcc cccaagctct gaggcggaca 3000
gcttctgggg gacggacgga gcagggcatg agcagaagca cgagtgtcac ttcacaaata 3060
15 tccaatgggt cacacatgtc ttatacataa cttaataatt gagagtggca attccgctgg 3120
agctgtctgc caaaagaaac tgcctacaga catcatcaca gcagcctcct cacttgggta 3180
ctacagtgtg gaagctgagt gcatatggta tattttattc atttttgtaa agcgttctgt 3240
20 tttgngttta ctaattggga tgncatagta cttggctncc cgggt 3285

```

```

<210> 10
25 <211> 1005
<212> PRT
30 <213> Homo sapiens

```

```

<300>
35 <308> SpTrEMBL
<309> 2000-10-01
<313> (1)..(1005)
40 <400> 10

```

```

Leu Leu Ser Arg Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp
45 1 5 10 15
Pro Glu Ile Ala Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe
20 25 30
50 Thr Asp Leu Arg Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe
35 40 45
Ala Arg Asp Val Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser
50 55 60
55 Tyr Ser Gly Lys Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu
65 70 75 80

```

	Val	Lys	Phe	Leu	Gln	Arg	Ile	Lys	His	Pro	Asn	Ser	Ile	Glu	Tyr	Lys	
					85					90					95		
5	Gly	Cys	Tyr	Leu	Arg	Glu	His	Thr	Ala	Trp	Leu	Val	Met	Glu	Tyr	Cys	
				100					105					110			
	Leu	Gly	Ser	Ala	Ser	Asp	Leu	Leu	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	
			115					120					125				
10	Glu	Val	Glu	Ile	Ala	Ala	Ile	Thr	His	Gly	Ala	Leu	Gln	Gly	Leu	Ala	
		130					135					140					
	Tyr	Leu	His	Ser	His	Thr	Met	Ile	His	Arg	Asp	Ile	Lys	Ala	Gly	Asn	
15	145					150				155						160	
	Ile	Leu	Leu	Thr	Glu	Pro	Gly	Gln	Val	Lys	Leu	Ala	Asp	Phe	Gly	Ser	
				165						170					175		
20	Ala	Ser	Met	Ala	Ser	Pro	Ala	Asn	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	
				180					185					190			
	Met	Ala	Pro	Glu	Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	
			195					200					205				
25	Lys	Val	Asp	Val	Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	
		210					215					220					
	Arg	Lys	Pro	Pro	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	
30	225					230				235						240	
	Ile	Ala	Gln	Asn	Glu	Ser	Pro	Thr	Leu	Gln	Ser	Asn	Glu	Trp	Ser	Asp	
				245						250					255		
35	Tyr	Phe	Arg	Asn	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Asp	
				260					265					270			
	Arg	Pro	Thr	Ser	Glu	Glu	Leu	Leu	Lys	His	Ile	Phe	Val	Leu	Arg	Glu	
			275					280					285				
40	Arg	Pro	Glu	Thr	Val	Leu	Ile	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	
		290					295					300					
	Val	Arg	Glu	Leu	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Leu	Leu	
45	305					310				315						320	
	Phe	Gln	Glu	Ala	His	Asn	Gly	Pro	Ala	Val	Glu	Ala	Gln	Glu	Glu	Glu	
				325						330				335			
50	Glu	Glu	Gln	Asp	His	Gly	Val	Gly	Arg	Thr	Gly	Thr	Val	Asn	Ser	Val	
				340					345					350			
	Gly	Ser	Asn	Gln	Ser	Ile	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	
			355					360					365				
55	Ser	Ser	Ser	Val	Asn	Ser	Leu	Pro	Asp	Val	Ser	Asp	Asp	Lys	Ser	Glu	
		370					375					380					

	Leu	Asp	Met	Met	Glu	Gly	Asp	His	Thr	Val	Met	Ser	Asn	Ser	Ser	Val	
	385					390					395					400	
5	Ile	His	Leu	Lys	Pro	Glu	Glu	Glu	Asn	Tyr	Arg	Glu	Glu	Gly	Asp	Pro	
					405					410					415		
	Arg	Thr	Arg	Ala	Ser	Asp	Pro	Gln	Ser	Pro	Pro	Gln	Val	Ser	Arg	His	
				420					425					430			
10	Lys	Ser	His	Tyr	Arg	Asn	Arg	Glu	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	
			435					440					445				
	Ser	Leu	Val	Thr	Arg	Gln	Met	Gln	Glu	His	Glu	Gln	Asp	Ser	Glu	Leu	
15		450					455					460					
	Arg	Glu	Gln	Met	Ser	Gly	Tyr	Lys	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	
	465					470				475						480	
20	Gln	Leu	Met	Thr	Leu	Glu	Asn	Lys	Leu	Lys	Ala	Glu	Met	Asp	Glu	His	
					485					490					495		
	Arg	Leu	Arg	Leu	Asp	Lys	Asp	Leu	Glu	Thr	Gln	Arg	Asn	Asn	Phe	Ala	
				500					505					510			
25	Ala	Glu	Met	Glu	Lys	Leu	Ile	Lys	Lys	His	Gln	Ala	Ala	Met	Glu	Lys	
			515					520					525				
	Glu	Ala	Lys	Val	Met	Ser	Asn	Glu	Glu	Lys	Lys	Phe	Gln	Gln	His	Ile	
30		530					535					540					
	Gln	Ala	Gln	Gln	Lys	Lys	Glu	Leu	Asn	Ser	Phe	Leu	Glu	Ser	Gln	Lys	
	545					550					555					560	
35	Arg	Glu	Tyr	Lys	Leu	Arg	Lys	Glu	Gln	Leu	Lys	Glu	Glu	Leu	Asn	Glu	
					565					570					575		
	Asn	Gln	Ser	Thr	Pro	Lys	Lys	Glu	Lys	Gln	Glu	Trp	Leu	Ser	Lys	Gln	
				580					585					590			
40	Lys	Glu	Asn	Ile	Gln	His	Phe	Gln	Ala	Glu	Glu	Glu	Ala	Asn	Leu	Leu	
			595					600					605				
	Arg	Arg	Gln	Arg	Gln	Tyr	Leu	Glu	Leu	Glu	Cys	Arg	Arg	Phe	Lys	Arg	
45		610					615					620					
	Arg	Met	Leu	Leu	Gly	Arg	His	Asn	Leu	Glu	Gln	Asp	Leu	Val	Arg	Glu	
	625					630					635					640	
50	Glu	Leu	Asn	Lys	Arg	Gln	Thr	Gln	Lys	Asp	Leu	Glu	His	Ala	Met	Leu	
					645					650					655		
	Leu	Arg	Gln	His	Glu	Ser	Met	Gln	Glu	Leu	Glu	Phe	Arg	His	Leu	Asn	
				660					665					670			
55	Thr	Ile	Gln	Lys	Met	Arg	Cys	Glu	Leu	Ile	Arg	Leu	Gln	His	Gln	Thr	
			675					680					685				

	Glu	Leu	Thr	Asn	Gln	Leu	Glu	Tyr	Asn	Lys	Arg	Arg	Glu	Arg	Glu	Leu	
	690						695					700					
5	Arg	Arg	Lys	His	Val	Met	Glu	Val	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	
	705					710					715					720	
	Ser	Lys	Glu	Leu	Gln	Ile	Lys	Lys	Gln	Phe	Gln	Asp	Thr	Cys	Lys	Ile	
					725					730					735		
10	Gln	Thr	Arg	Gln	Tyr	Lys	Ala	Leu	Arg	Asn	His	Leu	Leu	Glu	Thr	Thr	
				740					745					750			
	Pro	Lys	Ser	Glu	His	Lys	Ala	Val	Leu	Lys	Arg	Leu	Lys	Glu	Glu	Gln	
15			755					760					765				
	Thr	Arg	Lys	Leu	Ala	Ile	Leu	Ala	Glu	Gln	Tyr	Asp	His	Ser	Ile	Asn	
	770						775					780					
20	Glu	Met	Leu	Ser	Thr	Gln	Ala	Leu	Arg	Leu	Asp	Glu	Ala	Gln	Glu	Ala	
	785					790					795					800	
	Glu	Cys	Gln	Val	Leu	Lys	Met	Gln	Leu	Gln	Gln	Glu	Leu	Glu	Leu	Leu	
					805					810					815		
25	Asn	Ala	Tyr	Gln	Ser	Lys	Ile	Lys	Met	Gln	Ala	Glu	Ala	Gln	His	Asp	
				820					825					830			
	Arg	Glu	Leu	Arg	Glu	Leu	Glu	Gln	Arg	Val	Ser	Leu	Arg	Arg	Ala	Leu	
30			835					840					845				
	Leu	Glu	Gln	Lys	Ile	Glu	Glu	Glu	Met	Leu	Ala	Leu	Gln	Asn	Glu	Arg	
	850						855					860					
35	Thr	Glu	Arg	Ile	Arg	Ser	Leu	Leu	Glu	Arg	Gln	Ala	Arg	Glu	Ile	Glu	
	865					870					875					880	
	Ala	Phe	Asp	Ser	Glu	Ser	Met	Arg	Leu	Gly	Phe	Ser	Asn	Met	Val	Leu	
					885					890					895		
40	Ser	Asn	Leu	Ser	Pro	Glu	Ala	Phe	Ser	His	Ser	Tyr	Pro	Gly	Ala	Ser	
				900					905					910			
	Gly	Trp	Ser	His	Asn	Pro	Thr	Gly	Gly	Pro	Gly	Pro	His	Trp	Gly	His	
45			915					920					925				
	Pro	Met	Gly	Gly	Pro	Pro	Gln	Ala	Trp	Gly	His	Pro	Met	Gln	Gly	Gly	
	930						935					940					
50	Pro	Gln	Pro	Trp	Gly	His	Pro	Ser	Gly	Pro	Met	Gln	Gly	Val	Pro	Arg	
	945					950					955					960	
	Gly	Ser	Ser	Met	Gly	Val	Arg	Asn	Ser	Pro	Gln	Ala	Leu	Arg	Arg	Thr	
					965					970					975		
55	Ala	Ser	Gly	Gly	Arg	Thr	Glu	Gln	Gly	Met	Ser	Arg	Ser	Thr	Ser	Val	
				980					985					990			

Thr Ser Gln Ile Ser Asn Gly Ser His Met Ser Tyr Thr
 995 1000 1005

5 <210> 11
 <211> 1576
 10 <212> DNA
 <213> artificial sequence
 15 <220>
 <223> RNAi fragment T17E9.1a (kin-18)
 <400> 11
 20 cgaaaaccag cagaagagcg aatgtcagct gaagaatgct ttcgacatcc attcattcaa 60
 cggctctcgcc catcagacac aattcaggaa ctcatcaga gaacgaaaaa tatggtatta 120
 gagttggata attttcaata caaaaagatg agaaaactca tgtatttgga tgaaacagaa 180
 25 ggaaaagaag gaagtgaagg aaatggagca tctgatgatt tagattttca tggaaatgaa 240
 gctaattcaa ttggaagagg tagtttttaa aattcaaagt gaaaatatta atatcttgga 300
 30 ataattttta taatattgct ttaaaccctc agcttttttt tgcagactct atcccttagt 360
 tgttcgtttt ccattctatc tcgttttcag caggagattc tgcgtcatct cgaagtgcct 420
 ctcttacttc tttccgatca atgcagagta gtggaggagc tggctcttta gtgtccacca 480
 35 atacgacggg tgctatggat aatgtgcatg gtactgtact gttttttttg ttttaggaat 540
 ggctttatta tttcctgcaa agttcaaaaa ttccatttat tttagttttt ctctcgaaat 600
 40 tcatcgcgca acattgagaa tctttcaaaa ttttcaggat cctctggata cggtaatgga 660
 agtagttcga cgacgagctc cgacgccgc cgtcctccaa ttccttcgca aatgctctct 720
 tctacatcaa cgtctggtgt tggaactatg ccgagtcatt gatcagttgg agcatcgatt 780
 45 acggcgatcg cagtcaatcc aacaccgtct ccttcagaac ctatcccaac atcacaacca 840
 acatcgaaat cagaatcatc ttctatactc gaaactgcac acgatgatcc tttggacacg 900
 50 tcgatacgtg ctccagtgaag agacttgcatt atgccgcatt gagcagtcaa ggaacgaata 960
 gccacgttgc aaaatcacia attcgcgacg cttcgttccc agagaataat caatcaggaa 1020
 caagaagaat atacgaaaga gaacaatatg tatgagcaaaa tgagcaagta caagcatcta 1080
 55 cgacaagcac atcaciaaga gctccaacia tttgaagaac gatgtgcatt agatagagag 1140

caactgctg tgaaaatgga tcgagaactc gaacaattga caacgacata ctcgaaagaa 1200
aagatgagag tgaggtgttc acagaataat gaactagaca aacggaaaaa agatatcgaa 1260
5 gatggggaga aaaagatgaa aaagacgaaa aatagtcaaa atcagcagca gatgaaactg 1320
tattcagcgc aacaattgaa agaatacaag tataacaagg aggcacagaa aacagtgaga 1380
attcactttt atttgatttc tgtaaagaaa ttatacgaaa tttagacttt ataaattttt 1440
10 aaatatgaaa gttctggtca ctttttcagc tgcttctcca cttttttcaa agtttattat 1500
ttagtcttga ataatttttt aaaaaatgtc ctaaaccaag aattttcagc gattacgaag 1560
15 tctgaacatg cctcga 1576

<210> 12

20 <211> 20

<212> DNA

25 <213> artificial sequence

<220>

30 <223> primer

<400> 12

cgaaaaccag cagaagagcg

20

35 <210> 13

<211> 21

<212> DNA

40 <213> artificial sequence

<220>

45 <223> primer

<400> 13

tcgaggcatg ttcagacttc g

21

50